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(54) CBS2 polypeptides, members of the guanine exchange factor family

(57) CSB2 polypeptides and polynucleotides and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing CSB2 polypeptides and polynucleotides in therapy, and diagnostic assays for such.

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Description

Field of the Invention

This invention relates to newly identified polypeptides and polynucleotides encoding such polypeptides, to their use in therapy and in identifying compounds which may be agonists, antagonists and /or inhibitors which are potentially useful in therapy, and to production of such polypeptides and polynucleotides.

Background of the Invention

The drug discovery process is currently undergoing a fundamental revolution as it embraces 'functional genomics', that is, high throughput genome- or gene-based biology. This approach as a means to identify genes and gene products as therapeutic targets is rapidly superceding earlier approaches based on 'positional cloning'. A phenotype, that is a biological function or genetic disease, would be identified and this would then be tracked back to the responsible gene, based on its genetic map position.

Functional genomics relies heavily on high-throughput DNA sequencing technologies and the various tools of bioinformatics to identify gene sequences of potential interest from the many molecular biology databases now available. There is a continuing need to identify and characterise further genes and their related polypeptides/proteins, as targets for drug discovery.

Summary of the Invention

The present invention relates to CSB2, in particular CSB2 polypeptides and CSB2 polynucleotides, recombinant materials and methods for their production. In another aspect, the invention relates to methods for using such polypeptides and polynucleotides, including the treatment of cancer, heart hypertrophy, heart failure, ischaemia, arrythmia, hypertension, atherosclerosis, restenosis, chronic and acute inflammation, cerebral stroke, brain diseases, rheumatoid arthritis, Romano-Ward syndrome, generalised gangliosidis type I, Sotos syndrome and Laurence-Moon-Bardet-Biel syndrome, hereinafter referred to as "the Diseases", amongst others. In a further aspect, the invention relates to methods for identifying agonists and antagonists/inhibitors using the materials provided by the invention, and treating conditions associated with CSB2 imbalance with the identified compounds. In a still further aspect, the invention relates to diagnostic assays for detecting diseases associated with inappropriate CSB2 activity or levels.

Description of the Invention

In a first aspect, the present invention relates to CSB2 polypeptides. Such peptides include isolated polypeptides comprising an amino acid sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:2 or SEQ ID NO:6 over the entire length of SEQ ID NO:2 or SEQ ID NO:6. Such polypeptides include those comprising the amino acid of SEQ ID NO:2 or SEQ ID NO:6.

Further peptides of the present invention include isolated polypeptides in which the amino acid sequence has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:6 over the entire length of SEQ ID NO:2 or SEQ ID NO:6. Such polypeptides include the polypeptide of SEQ ID NO:2 and SEQ ID NO:6.

Further peptides of the present invention include isolated polypeptides encoded by a polynucleotide comprising the sequence contained in SEQ ID NO: 1 or SEQ ID NO:5.

The polypeptides shown in SEQ ID NO:2 and SEQ ID NO:6 are the products of alternatively spliced primary transcripts, comprising the cDNA sequences given in SEQ ID NO: 1 and SEQ ID NO:5.

Polypeptides of the present invention are members of the guanine nucleotide exchange factor (GEF) family of polypeptides. They are therefore of interest because GEF proteins regulate Ras superfamily GTPases which are involved in cytoskeletal organisation, cell growth and proliferation, cell migration, cell adhesion, membrane trafficking, vesicles transport, mitosis, ADP-ribosylation and phospholipid metabolism . These properties are hereinafter referred to as CSB2 activity" or CSB2 polypeptide activity" or "biological activity of CSB2". Also included amongst these activities are antigenic and immunogenic activities of said CSB2 polypeptides, in particular the antigenic and immunogenic activities of the polypeptide of SEQ ID NO:2 or SEQ ID NO:6. Preferably, a polypeptide of the present invention exhibits at least one biological activity of CSB2.

The polypeptides of the present invention may be in the form of the "mature" protein or may be a part of a larger protein such as a fusion protein. It is often advantageous to include an additional amino acid sequence which contains

secretory or leader sequences, pro-sequences, sequences which aid in purification such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The present invention also includes include variants of the aforementioned polypeptides, that is polypeptides that vary from the referents by conservative amino acid substitutions, whereby a residue is substituted by another with like characteristics. Typical such substitutions are among Ala, Val, Leu and Ile; among Ser and Thr, among the acidic residues Asp and Glu; among Asn and Gln; and among the basic residues Lys and Arg; or aromatic residues Phe and Tyr. Particularly preferred are variants in which several, 5-10, 1-5, 1-3, 1-2 or 1 amino acids are substituted, deleted, or added in any combination.

Polypeptides of the present invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

In a further aspect, the present invention relates to CSB2 polynucleotides. Such polynucleotides include isolated polynucleotides comprising a nucleotide sequence encoding a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, to the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:6, over the entire length of SEQ ID NO:2 or SEQ ID NO:6. In this regard, polypeptides which have at least 97% identity are highly preferred, whilst those with at least 98-99% identity are more highly preferred, and those with at least 99% identity are most highly preferred. Such polynucleotides include a polynucleotide comprising the nucleotide sequence contained in SEQ ID NO:1 or SEQ ID NO:5 encoding the polypeptide of SEQ ID NO:2 or SEQ ID NO:6 respectively.

Further polynucleotides of the present invention include isolated polynucleotides comprising a nucleotide sequence that has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, to a nucleotide sequence encoding a polypeptide of SEQ ID NO:2 or SEQ ID NO:6, over the entire coding region. In this regard, polynucleotides which have at least 97% identity are highly preferred, whilst those with at least 98-99% identity are more highly preferred, and those with at least 99% identity are most highly preferred.

Further polynucleotides of the present invention include isolated polynucleotides comprising a nucleotide sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, to SEQ ID NO:1 or SEQ ID NO:5 over the entire length of SEQ ID NO: 1 or SEQ ID NO: 5. In this regard, polynucleotides which have at least 97% identity are highly preferred, whilst those with at least 98-99% identiy are more highly preferred, and those with at least 99% identity are most highly preferred. Such polynucleotides include a polynucleotide comprising the polynucleotide of SEQ ID NO:1 or SEQ ID NO:5 as well as the polynucleotide of SEQ ID NO:1 or SEQ ID NO:5.

The invention also provides polynucleotides which are complementary to all the above described polynucleotides.

The nucleotide sequence of SEQ ID NO: shows homology with Netl (Chan, AM et al, Oncogene 12(6) p1259-1266, 1996). The nucleotide sequence of SEQ ID NO:1 is a cDNA sequence and comprises a polypeptide encoding sequence (nucleotide 134 to 1639) encoding a polypeptide of 526 amino acids, the polypeptide of SEQ ID NO:2. The nucleotide sequence encoding the polypeptide of SEQ ID NO:2 may be identical to the polypeptide encoding sequence contained in SEQ ID NO:1 or it may be a sequence other than the one contained in SEQ ID NO:1, which, as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:2. The polypeptide of the SEQ ID NO:2 is structurally related to other proteins of the guanine nucleotide exchange factor (GEF) family, having homology and/or structural similarity with Netl (Chan, AM et al, Oncogene 12(6) p1259-1266, 1996).

The nucleotide sequence of SEQ ID NO:5 shows homology with Netl (Chan, AM et al, Oncogene 12(6) p1259-1266, 1996). The nucleotide sequence of SEQ ID NO:5 is a cDNA sequence and comprises a polypeptide encoding sequence (nucleotide 73 to 1746) encoding a polypeptide of 558 amino acids, the polypeptide of SEQ ID NO:6. The nucleotide sequence encoding the polypeptide of SEQ ID NO:6 may be identical to the polypeptide encoding sequence contained in SEQ ID NO:5 or it may be a sequence other than the one contained in SEQ ID NO:5, which, as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:6. The polypeptide of the SEQ ID NO:6 is structurally related to other proteins of the guanine nucleotide exchange factor (GEF) family, having homology and/or structural similarity with Netl (Chan, AM et al, Oncogene 12(6) p1259-1266, 1996).

Preferred polypeptides and polynucleotides of the present invention are expected to have, *inter alia,* similar biological functions/properties to their homologous polypeptides and polynucleotides. Furthermore, preferred polypeptides and polynucleotides of the present invention have at least one CSB2 activity.

The present invention also relates to partial or other polynucleotide and polypeptide sequences which were first identified prior to the determination of the corresponding full length sequences of SEQ ID NO:1 and SEQ ID NO:5 and their corresponding polypeptide sequences SEQ ID NO:2 and SEQ ID NO:6.

Accordingly, in a further aspect, the present invention provides for an isolated polynucleotide which:

(a) comprises a nucleotide sequence which has at least 70% identity, preferably at least 80% identity, more pref-

erably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% identity to SEQ ID NO:3 over the entire length of SEQ ID NO:3;

(b) has a nucleotide sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% identity, to SEQ ID NO:3 over the entire length of SEQ ID NO:3;

(c) the polynucleotide of SEQ ID NO:3; or

(d) a nucleotide sequence encoding a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% identity, to the amino acid sequence of SEQ ID NO:4, over the entire length of SEQ ID NO:4;

as well as the polynucleotide of SEQ ID NO:3.

The present invention further provides for a polypeptide which:

(a) comprises an amino acid sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:4 over the entire length of SEQ ID NO:4;

(b) has an amino acid sequence which is at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to the amino acid sequence of SEQ ID NO:4 over the entire length of SEQ ID NO:4;

(c) comprises the amino acid of SEQ ID NO:4; and

(d) is the polypeptide of SEQ ID NO:4;

as well as polypeptides encoded by a polynucleotide comprising the sequence contained in SEQ ID NO:3.

The nucleotide sequence of SEQ ID NO:3 and the peptide sequence encoded thereby are derived from EST (Expressed Sequence Tag) sequences. It is recognised by those skilled in the art that there will inevitably be some nucleotide sequence reading errors in EST sequences (see Adams, M.D. *et al,* Nature 377 (supp) 3, 1995). Accordingly, the nucleotide sequence of SEQ ID NO:3 and the peptide sequence encoded therefrom are therefore subject to the same inherent limitations in sequence accuracy. Furthermore, the peptide sequence encoded by SEQ ID NO:3 comprises a region of identity or close homology and/or close structural similarity (for example a conservative amino acid difference) with the closest homologous or structurally similar protein.

Polynucleotides of the present invention may be obtained, using standard cloning and screening techniques, from a cDNA library derived from mRNA in cells of human brain, T cell lymphoma, melanoma, foetal dura mater, foetal heart, prostate, endometrial tumour, activated T cell, substantia nigra, testes, apoptotic T cell, foetal liver, multiple sclerosis, parathyroid tumour, activated monocyte, primary dendritic cells, adipose, resting T cell, lung, helper T cell, pancreas islet cell, using the expressed sequence tag (EST) analysis (Adams, M.D., *et al.* Science (1991) 252:1651-1656; Adams, M.D. *et al.,* Nature, (1992) *355*:632-634; Adams, M.D., *et al.,* Nature (1995) 377 Supp:3-174). Polynucleotides of the invention can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available techniques.

When polynucleotides of the present invention are used for the recombinant production of polypeptides of the present invention, the polynucleotide may include the coding sequence for the mature polypeptide, by itself; or the coding sequence for the mature polypeptide in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence which facilitates purification of the fused polypeptide can be encoded. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.,* Proc Natl Acad Sci USA (1989) 86:821-824, or is an HA tag. The polynucleotide may also contain non-coding 5' and 3' sequences, such as transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

Further embodiments of the present invention include polynucleotides encoding polypeptide variants which comprise the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:6 and in which several, for instance from 5 to 10, 1 to 5, 1 to 3, 1 to 2 or 1, amino acid residues are substituted, deleted or added, in any combination.

Polynucleotides which are identical or sufficiently identical to a nucleotide sequence contained in SEQ ID NO:1 or SEQ ID NO:5, may be used as hybridization probes for cDNA and genomic DNA or as primers for a nucleic acid amplification (PCR) reaction, to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes (including genes encoding homologs and orthologs from species other than human) that have a high sequence similarity to SEQ ID NO: 1 or SEQ ID NO:5. Typically these nucleotide sequences are 70% identical, preferably 80% identical, more preferably 90% identical, most preferably 95% identical to that of the referent. The probes or primers will generally comprise at least 15 nucleotides, preferably, at least 30 nucleotides and may have at least 50 nucleotides. Particularly preferred probes will have between 30 and 50

nucleotides.

A polynucleotide encoding a polypeptide of the present invention, including homologs and orthologs from species other than human, may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions with a labeled probe having the sequence of SEQ ID NO: 1, SEQ ID NO:5 or fragments thereof; and isolating full-length cDNA and genomic clones containing said polynucleotide sequence. Such hybridization techniques are well known to the skilled artisan: Preferred stringent hybridization conditions include overnight incubation at 42°C in a solution comprising: 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10 % dextran sulfate, and 20 microgram/ml denatured, sheared salmon sperm DNA; followed by washing the filters in 0. lx SSC at about 65°C. Thus the present invention also includes polynucleotides obtainable by screening an appropriate library under stingent hybridization conditions with a labeled probe having the sequence of SEQ ID NO:1, SEQ ID NO:5 or fragments thereof.

The skilled artisan will appreciate that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide is cut short at the 5' end of the cDNA. This is a consequence of reverse transcriptase, an enzyme with inherently low 'processivity' (a measure of the ability of the enzyme to remain attached to the template during the polymerisation reaction), failing to complete a DNA copy of the mRNA template during 1st strand cDNA synthesis.

There are several methods available and well known to those skilled in the art to obtain full-length cDNAs, or extend short cDNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman et al., PNAS USA 85, 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon™ technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon™ technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the 'missing' 5' end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using 'nested' primers, that is, primers designed to anneal within the amplified product (typically an adaptor specific primer that anneals further 3' in the adaptor sequence and a gene specific primer that anneals further 5' in the known gene sequence). The products of this reaction can then be analysed by DNA sequencing and a full-length cDNA constructed either by joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the design of the 5' primer.

Recombinant polypeptides of the present invention may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems which comprise a polynucleotide or polynucleotides of the present invention, to host cells which are genetically engineered with such expression sytems and to the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof for polynucleotides of the present invention. Introduction of polynucleotides into host cells can be effected by methods described in many standard laboratory manuals, such as Davis et al., Basic Methods in Molecular Biology (1986) and Sambrook *et al.,* Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989). Preferred such methods include, for instance, calcium phosphate transfection, DEAE-dextran mediated transfection, transvection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection.

Representative examples of appropriate hosts include bacterial cells, such as *Streptococci, Staphylococci, E. coli, Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, HEK 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used, for instance, chromosomal, episomal and virus-derived systems, e.g., vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression systems may contain control regions that regulate as well as engender expression. Generally, any system or vector which is able to maintain, propagate or express a polynucleotide to produce a polypeptide in a host may be used. The appropriate nucleotide sequence may be inserted into an expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.,* Molecular Cloning, A Laboratory Manual (supra). Appropriate secretion signals may be incorporated into the desired polypeptide to allow secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the polypeptide or they may be heterologous signals.

If a polypeptide of the present invention is to be expressed for use in screening assays, it is generally preferred

that the polypeptide be produced at the surface of the cell. In this event, the cells may be harvested prior to use in the screening assay. If the polypeptide is secreted into the medium, the medium can be recovered in order to recover and purify the polypeptide. If produced intracellularly, the cells must first be lysed before the polypeptide is recovered.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during isolation and or purification.

This invention also relates to the use of polynucleotides of the present invention as diagnostic reagents. Detection of a mutated form of the gene characterised by the polynucleotide of SEQ ID NO:1 or SEQ ID NO:5 which is associated with a dysfunction will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, or susceptibility to a disease, which results from under-expression, over-expression or altered expression of the gene. Individuals carrying mutations in the gene may be detected at the DNA level by a variety of techniques.

Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification techniques prior to analysis. RNA or cDNA may also be used in similar fashion. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to labeled CSB2 nucleotide sequences. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in electrophoretic mobility of DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing (ee, e.g., Myers *et al.,* Science (1985) 230:1242). Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method (see Cotton *et al.,* Proc Natl Acad Sci USA (1985)85: 43974401). In another embodiment, an array of oligonucleotides probes comprising CSB2 nucleotide sequence or fragments thereof can be constructed to conduct efficient screening of e.g., genetic mutations. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability (see for example: M.Chee et al., Science, Vol 274, pp 610-613 (1996)).

The diagnostic assays offer a process for diagnosing or determining a susceptibility to the Diseases through detection of mutation in the CSB2 gene by the methods described. In addition, such diseases may be diagnosed by methods comprising determining from a sample derived from a subject an abnormally decreased or increased level of polypeptide or mRNA. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, nucleic acid amplification, for instance PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as a polypeptide of the present invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Thus in another aspect, the present invention relates to a diagonostic kit which comprises:

(a) a polynucleotide of the present invention, preferably the nucleotide sequence of SEQ ID NO: 1, SEQ ID NO:5 or fragments thereof;

(b) a nucleotide sequence complementary to that of (a);

(c) a polypeptide of the present invention, preferably the polypeptide of SEQ ID NO:2, SEQ ID NO:6 or fragments thereof; or

(d) an antibody to a polypeptide of the present invention, preferably to the polypeptide of SEQ ID NO:2 or SEQ ID NO:6.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or suspectability to a disease, particularly cancer, heart hypertrophy, heart failure, ischaemia, arrythmia, hypertension, atherosclerosis, restenosis, chronic and acute inflammation, cerebral stroke, brain diseases, rheumatoid arthritis, Romano-Ward syndrome, generalised gangliosidis type I, Sotos syndrome and Laurence-Moon-Bardet-Bield syndrome, among others.

The nucleotide sequences of the present invention are also valuable for chromosome localisation. The sequence is specifically targeted to, and can hybridize with, a particular location on an individual human chromosome. The mapping of relevant sequences to chromosomes according to the present invention is an important first step in correlating those sequences with gene associated disease. Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data

are found in, for example, V. McKusick, Mendelian Inheritance in Man (available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (coinheritance of physically adjacent genes).

The differences in the cDNA or genomic sequence between affected and unaffected individuals can also be determined. If a mutation is observed in some or all of the affected individuals but not in any normal individuals, then the mutation is likely to be the causative agent of the disease.

The gene of the present invention maps to human chromosome 3p21-p14 between markers D3S 1300 and D3S1600.

The nucleotide sequences of the present invention are also valuable for tissue localisation. Such techniques allow the determination of expression patterns of the CSB2 polypeptides in tissues by detection of the mRNAs that encode them. These techniques include in situ hybridziation techniques and nucleotide amplification techniques, for example PCR. Such techniques are well known in the art. Results from these studies provide an indication of the normal functions of the polypeptides in the organism. In addition, comparative studies of the normal expression pattern of CSB2 mRNAs with that of mRNAs encoded by a mutant CSB2 gene provide valuable insights into the role of mutant CSB2 polypeptides, or that of inappropriate expression of normal CSB2 polypeptides, in disease. Such inappropriate expression may be of a temporal, spatial or simply quantitative nature.

The polypeptides of the invention or their fragments or analogs thereof, or cells expressing them, can also be used as immunogens to produce antibodies immunospecific for polypeptides of the present invention. The term "immunospecific" means that the antibodies have substantially greater affinity for the polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against polypeptides of the present invention may be obtained by administering the polypeptides or epitope-bearing fragments, analogs or cells to an animal, preferably a non-human animal, using routine protocols. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler, G. and Milstein, C., Nature (1975) 256:495497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.,* Immunology Today (1983) 4:72) and the EBV-hybridoma technique (Cole *et al.,* Monoclonal Antibodies and Cancer Therapy, 77-96, Alan R. Liss, Inc., 1985).

Techniques for the production of single chain antibodies, such as those described in U.S. Patent No. 4,946,778, can also be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptide or to purify the polypeptides by affulity chromatography.

Antibodies against polypeptides of the present invention may also be employed to treat the Diseases, amongst others.

In a further aspect, the present invention relates to genetically engineered soluble fusion proteins comprising a polypeptide of the present invention, or a fragment thereof, and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE). Preferred as an immunoglobulin is the constant part of the heavy chain of human IgG, particularly IgG1, where fusion takes place at the hinge region. In a particular embodiment, the Fc part can be removed simply by incorporation of a cleavage sequence which can be cleaved with blood clotting factor Xa. Furthermore, this invention relates to processes for the preparation of these fusion proteins by genetic engineering, and to the use thereof for drug screening, diagnosis and therapy. A further aspect of the invention also relates to polynucleotides encoding such fusion proteins. Examples of fusion protein technology can be found in International Patent Application Nos. W094/29458 and WO94/22914.

Another aspect of the invention relates to a method for inducing an immunological response in a mammal which comprises inoculating the mammal with a polypeptide of the present invention, adequate to produce antibody and/or T cell immune response to protect said animal from the Diseases hereinbefore mentioned, amongst others. Yet another aspect of the invention relates to a method of inducing immunological response in a mammal which comprises, delivering a polypeptide of the present invention *via* a vector directing expression of the polynucleotide and coding for the polypeptide *in vivo* in order to induce such an immunological response to produce antibody to protect said animal from diseases.

A further aspect of the invention relates to an immunological/vaccine formulation (composition) which, when introduced into a mammalian host, induces an immunological response in that mammal to a polypeptide of the present invention wherein the composition comprises a polypeptide or polynucleotide of the present invention. The vaccine formulation may further comprise a suitable carrier. Since a polypeptide may be broken down in the stomach, it is preferably administered parenterally (for instance, subcutaneous, intramuscular, intravenous, or intradermal injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation instonic with the blood of the recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening

agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

Polypeptides of the present invention are responsible for one or more biological functions, including one or more disease states, in particular the Diseases hereinbefore mentioned. It is therefore desirous to devise screening methods to identify compounds which stimulate or which inhibit the function of the polypeptide. Accordingly, in a further aspect, the present invention provides for a method of screening compounds to identify those which stimulate or which inhibit the function of the polypeptide. In general, agonists or antagonists may be employed for therapeutic and prophylactic purposes for such Diseases as hereinbefore mentioned. Compounds may be identified from a variety of sources, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. Such agonists, antagonists or inhibitors so-identified may be natural or modified substrates, ligands, receptors, enzymes, etc., as the case may be, of the polypeptide; or may be structural or functional mimetics thereof (see Coligan *et al.*, Current Protocols in Immunology 1(2):Chapter 5 (1991)).

The screening method may simply measure the binding of a candidate compound to the polypeptide, or to cells or membranes bearing the polypeptide, or a fusion protein thereof by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve competition with a labeled competitor. Further, these screening methods may test whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells bearing the polypeptide. Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Constitutively active polypeptides may be employed in screening methods for inverse agonists or inhibitors, in the absence of an agonist or inhibitor, by testing whether the candidate compound results in inhibition of activation of the polypeptide. Further, the screening methods may simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide of the present invention, to form a mixture, measuring CSB2 activity in the mixture, and comparing the CSB2 activity of the mixture to a standard. Fusion proteins, such as those made from Fc portion and CSB2 polypeptide, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists for the polypeptide of the present invention (see D. Bennett *et al.*, J Mol Recognition, 8:52-58 (1995); and K. Johanson *et al.*, J Biol Chem, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies to the polypeptide of the present invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the an. This can be used to discover agents which may inhibit or enhance the production of polypeptide (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

The polypeptide may be used to identify membrane bound or soluble receptors, if any, through standard receptor binding techniques known in the art. These include, but are not limited to, ligand binding and crosslinking assays in which the polypeptide is labeled with a radioactive isotope (for instance, ^{125}I), chemically modified (for instance, biotinylated), or fused to a peptide sequence suitable for detection or purification, and incubated with a source of the putative receptor (cells, cell membranes, cell supematants, tissue extracts, bodily fluids). Other methods include biophysical techniques such as surface plasmon resonance and spectroscopy. These screening methods may also be used to identify agonists and antagonists of the polypeptide which compete with the binding of the polypeptide to its receptors, if any. Standard methods for conducting such assays are well understood in the art.

Examples of potential polypeptide antagonists include antibodies or, in some cases, oligonucleotides or proteins which are closely related to the ligands, substrates, receptors, enzymes, etc., as the case may be, of the polypeptide, e.g., a fragment of the ligands, substrates, receptors, enzymes, etc.; or small molecules which bind to the polypeptide of the present invention but do not elicit a response, so that the activity of the polypeptide is prevented.

Thus, in another aspect, the present invention relates to a screening kit for identifying agonists, antagonists, ligands, receptors, substrates, enzymes, etc. for polypeptides of the present invention; or compounds which decrease or enhance the production of such polypeptides, which comprises:

(a) a polypeptide of the present invention;
(b) a recombinant cell expressing a polypeptide of the present invention;
(c) a cell membrane expressing a polypeptide of the present invention; or
(d) antibody to a polypeptide of the present invention;

which polypeptide is preferably that of SEQ ID NO:2 or SEQ ID NO:6.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

It will be readily appreciated by the skilled artisan that a polypeptide of the present invention may also be used in a method for the structure-based design of an agonist, antagonist or inhibitor of the polypeptide, by:

(a) determining in the first instance the three-dimensional structure of the polypeptide;
(b) deducing the three-dimensional structure for the likely reactive or binding site(s) of an agonist, antagonist or inhibitor;
(c) synthesing candidate compounds that are predicted to bind to or react with the deduced binding or reactive site; and
(d) testing whether the candidate compounds are indeed agonists, antagonists or inhibitors. It will be further appreciated that this will normally be an iterative process.

In a further aspect, the present invention provides methods of treating abnormal conditions such as, for instance, cancer, heart hypertrophy, heart failure, ischaemia, arrythmia, hypertension, atherosclerosis, restenosis, chronic and acute inflammation, cerebral stroke, brain diseases, rheumatoid arthritis, Romano-Ward syndrome, generalised gangliosidis type I, Sotos syndrome and Laurence-Moon-Bardet-Bield syndrome, related to either an excess of, or an under-expression of, CSB2 polypeptide activity.

If the activity of the polypeptide is in excess, several approaches are available. One approach comprises administering to a subject in need thereof an inhibitor compound (antagonist) as hereinabove described, optionally in combination with a pharmaceutically acceptable carrier, in an amount effective to inhibit the function of the polypeptide, such as, for example, by blocking the binding of ligands, substrates, receptors, enzymes, etc., or by inhibiting a second signal, and thereby alleviating the abnormal condition. In another approach, soluble forms of the polypeptides still capable of binding the ligand, substrate, enzymes, receptors, etc. in competition with endogenous polypeptide may be administered. Typical examples of such competitors include fragments of the CSB2 polypeptide.

In still another approach, expression of the gene encoding endogenous CSB2 polypeptide can be inhibited using expression blocking techniques. Known such techniques involve the use of antisense sequences, either internally generated or externally administered (see, for example, O'Connor, J Neurochem (1991) 56:560 in Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Alternatively, oligonucleotides which form triple helices ("triplexes") with the gene can be supplied (see, for example, Lee *et al.*, Nucleic Acids Res (1979) 6:3073; Cooney *et al.*, Science (1988) 241:456; Dervan *et al.*, Science (1991) 251:1360). These oligomers can be administered *per se* or the relevant oligomers can be expressed *in vivo*. Synthetic antisense or triplex oligonucleotides may comprise modified bases or modified backbones. Examples of the latter include methylphosphonate, phosphorothioate or peptide nucleic acid backbones. Such backbones are incorporated in the antisense or triplex oligonucleotide in order to provide protection from degradation by nucleases and are well known in the art. Antisense and triplex molecules synthesised with these or other modified backbones also form part of the present invention.

In addition, expression of the CSB2 polypeptide may be prevented by using ribozymes specific to the CSB2 mRNA sequence. Ribozymes are catalytically active RNAs that can be natural or synthetic (see for example Usman, N, et al., Curr. Opin. Struct. Biol (1996) 6(4), 527-33.) Synthetic ribozymes can be designed to specifically cleave CSB2 mRNAs at selected positions thereby preventing translation of the CSB2 mRNAs into functional polypeptide. Ribozymes may be synthesised with a natural ribose phosphate backbone and natural bases, as normally found in RNA molecules. Alternatively the ribosymes may be synthesised with non-natural backbones to provide protection from ribonuclease degradation, for example, 2'-O-methyl RNA, and may contain modified bases.

For treating abnormal conditions related to an under-expression of CSB2 and its activity, several approaches are also available. One approach comprises administering to a subject a therapeutically effective amount of a compound which activates a polypeptide of the present invention, i.e., an agonist as described above, in combination with a pharmaceutically acceptable carrier, to thereby alleviate the abnormal condition. Alternatively, gene therapy may be employed to effect the endogenous production of CSB2 by the relevant cells in the subject. For example, a polynucleotide of the invention may be engineered for expression in a replication defective retroviral vector, as discussed above. The retroviral expression construct may then be isolated and introduced into a packaging cell transduced with a retroviral plasmid vector containing RNA encoding a polypeptide of the present invention such that the packaging cell now produces infectious viral particles containing the gene of interest. These producer cells may be administered to a subject for engineering cells *in vivo* and expression of the polypeptide *in vivo*. For an overview of gene therapy, see Chapter 20, Gene Therapy and other Molecular Genetic-based Therapeutic Approaches, (and references cited therein) in Human Molecular Genetics, T Strachan and A P Read, BIOS Scientific Publishers Ltd (1996). Another approach is to administer a therapeutic amount of a polypeptide of the present invention in combination with a suitable pharmaceutical carrier.

In a further aspect, the present invention provides for pharmaceutical compositions comprising a therapeutically effective amount of a polypeptide, such as the soluble form of a polypeptide of the present invention, agonist/antagonist peptide or small molecule compound, in combination with a pharmaceutically acceptable carrier or excipient. Such

carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The invention further relates to pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. Polypeptides and other compounds of the present invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

The composition will be adapted to the route of administration, for instance by a systemic or an oral route. Preferred forms of systemic administration include injection, typically by intravenous injection. Other injection routes, such as subcutaneous, intramuscular, or intraperitoneal, can be used. Alternative means for systemic administration include transmucosal and transdermal administration using penetrants such as bile salts or fusidic acids or other detergents. In addition, if a polypeptide or other compounds of the present invention can be formulated in an enteric or an encapsulated formulation, oral administration may also be possible. Administration of these compounds may also be topical and/or localized, in the form of salves, pastes, gels, and the like.

The dosage range required depends on the choice of peptide or other compounds of the present invention, the route of administration, the nature of the formulation, the nature of the subject's condition, and the judgment of the attending practitioner. Suitable dosages, however, are in the range of 0,1-100 µg/kg of subject. Wide variations in the needed dosage, however, are to be expected in view of the variety of compounds available and the differing efficiencies of various routes of administration. For example, oral administration would be expected to require higher dosages than administration by intravenous injection. Variations in these dosage levels can be adjusted using standard empirical routines for optimization, as is well understood in the art.

Polypeptides used in treatment can also be generated endogenously in the subject, in treatment modalities often referred to as "gene therapy" as described above. Thus, for example, cells from a subject may be engineered with a polynucleotide, such as a DNA or RNA, to encode a polypeptide *ex vivo,* and for example, by the use of a retroviral plasmid vector. The cells are then introduced into the subject.

Polynucleotide and polypeptide sequences form a valuable information resource with which to identify further sequences of similar homology. This is most easily facilitated by storing the sequence in a computer readable medium and then using the stored data to search a sequence database using well known searching tools, such as those in the GCG and Lasergene software packages . Accordingly, in a further aspect, the present invention provides for a computer readable medium having stored thereon a polynucleotide comprising the sequence of SEQ ID NO:1 or SEQ ID NO:5 and/or a polypeptide sequence encoded thereby.

The following definitions are provided to facilitate understanding of certain terms used frequently hereinbefore.

"Antibodies" as used herein includes polyclonal and monoclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, including the products of an Fab or other immunoglobulin expression library.

"Isolated" means altered "by the hand of man" from the natural state. If an "isolated" composition or substance occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living animal is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

"Polynucleotide" generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. "Polynucleotides" include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single-and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term "polynucleotide" also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

"Polypeptide" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and

they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, biotinylation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, Proteins - Structure and Molecular Properties, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., Post-translational Protein Modifications: Perspectives and Prospects, pgs. 1-12 in Post-translational Covalent Modification of Proteins, B. C. Johnson, Ed., Academic Press, New York, 1983; Seifter *et al.*, "Analysis for protein modifications and nonprotein cofactors", Meth Enzymol (1990) 182: 626-646 and Rattan *et al.*, "Protein Synthesis: Post-translational Modifications and Aging", Ann NY Acad Sci (1992) 663:48-62).

"Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis.

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in *(Computational Molecular Biology,* Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects,* Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data,* Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology,* von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer,* Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., SIAM *J. Applied Math., 48:* 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research 12(1):* 387 (1984)), BLASTP, BLASTN, and FASTA (Atschul, S.F. et al., *J. Molec. Biol. 215:* 403-410 (1990). The BLAST X program is publicly available from NCBI and other sources *(BLAST Manual,* Altschul, S., *et al.,* NCBI NLM NIH Bethesda, MD 20894; Altschul, S., *et al., J. Mol. Biol. 215:* 403-410 (1990). The well known Smith Waterman algorithm may also be used to determine identity.

Preferred parameters for polypeptide sequence comparison include the following:

1) Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)

Comparison matrix: BLOSSUM62 from Hentikoff and Hentikoff, Proc. Natl. Acad. Sci. USA. 89:10915-10919 (1992)
Gap Penalty: 12
Gap Length Penalty: 4

A program useful with these parameters is publicly available as the "gap" program from Genetics Computer Group, Madison WI. The aforementioned parameters are the default parameters for peptide comparisons (along with no penalty for end gaps).

Preferred parameters for polynucleotide comparison include the following:

1) Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)

Comparison matrix: matches = +10, mismatch = 0
Gap Penalty: 50
Gap Length Penalty: 3

Available as: The "gap" program from Genetics Computer Group, Madison WI. These are the default parameters for nucleic acid comparisons.

By way of example, a polynucleotide sequence of the present invention may be identical to the reference sequence of SEQ ID NO:1 or SEQ ID NO:5, that is be 100% identical, or it may include up to a certain integer number of nucleotide alterations as compared to the reference sequence. Such alterations are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. The number of nucleotide alterations is determined by multiplying the total number of nucleotides in SEQ ID NO: 1 or SEQ ID NO:5 by the numerical percent of the respective percent identity (divided by 100) and subtracting that product from said total number of nucleotides in SEQ ID NO:1 or SEQ ID NO:5, or:

$$n_x \leq x_n - (x_n \bullet y),$$

wherein $\mathbf{n_n}$ is the number of nucleotide alterations, $\mathbf{x_n}$ is the total number of nucleotides in SEQ ID NO: 1 or SEQ ID NO:5, and **y** is, for instance, 0.70 for 70%, 0.80 for 80%, 0.85 for 85%, 0.90 for 90%, 0.95 for 95%,etc., and wherein any non-integer product of $\mathbf{x_n}$ and **y** is rounded down to the nearest integer prior to subtracting it from x_n. Alterations of a polynucleotide sequence encoding the polypeptide of SEQ ID NO:2 or SEQ ID NO:6 may create nonsense, missense or frameshift mutations in this coding sequence and thereby alter the polypeptide encoded by the polynucleotide following such alterations.

Similarly, a polypeptide sequence of the present invention may be identical to the reference sequence of SEQ ID NO:2 or SEQ ID NO:6, that is be 100% identical, or it may include up to a certain integer number of amino acid alterations as compared to the reference sequence such that the % identity is less than 100%. Such alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. The number of amino acid alterations for a given % identity is determined by multiplying the total number of amino acids in SEQ ID NO:2 or SEQ ID NO:6 by the numerical percent of the respective percent identity(divided by 100) and then subtracting that product from said total number of amino acids in SEQ ID NO:2 or SEQ ID NO:6, or:

$$n_a \leq x_a \cdot (x_a \bullet y),$$

wherein $\mathbf{n_a}$ is the number of amino acid alterations, $\mathbf{x_a}$ is the total number of amino acids in SEQ ID NO:2 or SEQ ID NO:6, and y is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., and wherein any non-integer product of $\mathbf{x_a}$ and **y** is rounded down to the nearest integer prior to subtracting it from $\mathbf{x_a}$.

"Homolog" is a generic term used in the art to indicate a polynucleotide or polypeptide sequence possessing a high degree of sequence relatedness to a subject sequence. Such relatedness may be quantified by determining the degree of identity and/or similarity between the sequences being compared as hereinbefore described.

Falling within this generic term are the terms "ortholog", meaning a polynucleotide or polypeptide that is the functional equivalent of a polynucleotide or polypeptide in another species, and "paralog" meaning a functionally similar sequence when considered within the same species. Hence in the rat, for example, a member of the family of serotonin receptors is a paralog of the other members of the rat serotonin receptor family.

"Fusion protein" refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. In one example, EP-A-0 464 discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion protein is advantageous for use in therapy and diagnosis resulting in, for example, improved pharmacokinetic properties [see, e.g., EP-A 0232 262]. On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified.

All publications, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference as if each individual publication were specifically and individually indicated to be incorporated

by reference herein as though fully set forth.

SEQUENCE INFORMATION

SEQ ID NO:1

TAGAAGCCGGCTGTCGGTCTCCGTGTCGCCGCCGCCGCCCGGCATCGTGGAGCTGGGGCCCCCTTTTGCCTG
GGAGTTTTGTAGTCGCCTAGGGTCAGCGGTGACATCCCAAAGGGCAGGCCCGGCAGCCGCCATGGTGGCCAA
GGATTACCCCTTCTACCTCACGGTCAAGAGAGCGAACTGCAGCCTGGAGCTACCCCCGGCCAGCGGTCCGGC
CAAGGACGCTGAGGAGCCTAGTAATAAACGGGTCAAACCCCTTTCCCGAGTCACGTCGCTAGCAAACCTCAT
CCCGCCCGTGAAGGcCACGCCATTAAAGCGCTTCAGTCAAACCCTGCAGCGCTCCATTAGCTTCCGCAGTGA
GAGCCGCCCTGACATCCTCGCCCCCCGACCCTGGTCCAGAAATGCCGCCCCCTCGAGCACGAAACGGAGAGA
TAGCAAGCTGTGGAGTGAGACCTTCGATGTGTGCGTCAATCAGATGCTTACATCCAAGGAAATCAAACGTCA
GGAGGCGATCTTTGAGCTTTCCCAAGGAGAAGAAGACTTGATAGAAGACTTGAAATTAGCAAAAAAGGCCTA
TCATGACCCCATGCTGAAACTCTCCATAATGACAGAACAAGAGTTGAATCAAATTTTTGGAACACTGGACTC
TCTAATTCCTCTACATGAAGAGCTCCTTAGTCAGCTTCGAGATGTTAGGAAGCCTGATGGCTCGACTGAACA
TGTTGGTCCCATCCTCGTGGGCTGGCTCCCTTGCCTCAGCTCCTATGATAGCTACTGCAGCAATCAAGTAGC
CGCCAAAGCTCTGCTGGACCACAAAAAGCAAGATCACCGAGTCCAGGATTTCCTACAGCGATGTTTAGAATC
CCCCTTTAGCCGCAAACTAGATCTCTGGAATTTCCTCGATATTCCAAGAAGCCGCCTGGTAAAATACCCTCT
GCTTCTCCGAGAAATCTTGAGGCACACACCAAATGATAATCCAGATCAGCAGCACTTGGAAGAAGCTATAAA
TATCATTCAGGGAATTGTGGCAGAAATCAACACCAAGACTGGTGAATCTGAATGCCGCTATTATAAAGAGCG
GCTTCTTTACTTGGAAGAAGGCCAGAAAGACTCCCTGATCGACAGCTCTCGAGTCTTGTGTTGTCATGGTGA
ACTGAAGAACAATCGGGGCGTGAAACTGCATGTTTTCCTGTTCCAAGAAGTGCTTGTGATCACTCGAGCCGT
CACCCACAATGAGCAGCTTTGCTACCAGCTGTACCGTCAGCCAATCCCCGTGAAAGACCTCCTGCTGGAAGA
CCTCCAGGATGGAGAAGTGAGGCTGGGTGGCTCCCTGCGAGGGGCATTCAGCAACAATGAGAGAATTAAAAA
CTTCTTCAGAGTCAGTTTCAAAAATGGATCCCAAAGTCAGACCCACTCGCTACAAGCCAATGACACTTTCAA
CAAACAGCAGTGGCTTAACTGTATTCGTCAAGCCAAAGAAACAGTTTTGTGTGCTGCCGGGCAAGCTGGGGT
GCTTGACTCCGAGGGATCGTTCCTAAATCCCACCACCGGGAGCAGAGAGCTACAGGGAGAAACAAAACTTGA
GCAGATGGACCAATCGGACAGTGAGTCAGACTGTAGTATGGACACGAGTGAGGTCAGCCTCGACTGTGAGCG
CATGGAACAGACAGACTCTTCCTGTGGAAACAGCAGGCACGGTGAAAGTAACGTCTGACAGAAGCATGTGCA
CTTCGGGAAGCAGGCCTGCATCTTACCTGTACAGTATTTGCATTCCACAGATGGAACGGTTTGGAGAAGCAC
TTTTTCATACTTTTGTGAAAGTATACATGTTGGCCCAGTCTCTCGTATCTGTACCTTTGTCCCTAGTACTGT
AACTGCCAATCTGTCTGTGTAAGCTGGAATCTGTGGCAACTATTACCCTGTGTTGTATTTCCCAAGTGTCTG
GATGGATGGAGAGGTACTCAAACAAGTTACTTTCAGTTGTCCTGCTGGATTTTAAAAAAATAGAAAAAGAAT
CTCAAAACTACTGTTTTACATAGATTGTTTGAAGAGTCCTTCCTCTTGTGCTTCTGTACCACTTTCCCAGCT
CTTAGATGTGGTAGCTAAAGGCACGGAATTTAGACGGCCTTGTAAATAGGGCATGAGGAACTCATCTGTGTA
TTGGGATGGTATTAGAGAGAGAATCAGGAAAGACCAACTCATGAAGTGAACTTGGTTTGATCTTACTCAACT
AGAAAGCTTGAAAACATCCCTGGGGATTCTGAAGGCTTAATTTTGCAAAGGAGGATGCATTGTCTGAACTTT
GCAACTTCATCCAGTGCAAGTTTGATGCAAGAATGTATTAGGACATAAAATAGAGGCTGACCTTAAAAGGGC
CAGGACAGAAGCGGCTGCCAGCTCTGAATCTTTAACTGAAATGCACATGGCACCAGGAGGTGTCTCTCATAG
TTGGTTGCTAGCCTAAAACATCAGAATAGAACCCAAAGGGCTTAGGAAGGCCTGCCAGGATAACAAGAAGGC
CCTGTATTCATTGTGTTTCATCTGCCTAGGCCTACTCATTATTTTAGAGAATGAATGAAGCAACAAGGAAGA
GAGACCATGACTCTATCGATGACACTGTTTATAGAAACACAGGAGAGGAAGAATTTGGAATGAAAAGCACTT
CGTCAGAACCTTCTGTGGGAGCCATTGAGAGAAAAGCATGGTCCAGTGCCTTCTGAGAAAGGCCAGAGCTTT
GGGCTTTCCTGCTCTGCTTTTGGGTCGTCAATTTGCCATCTCTGGTTCTGTGCTATAATCAGAATTGTAATT
ATGTTCTCCAGAGGCCAATTTCATTAACTCTGATTAATTAGAATCAGCTAGCCAGATTAGTAACCTCTTTGT
CCAGCCTTGATTTACAGTGCAGGGTAAAGTGCAGACCTTAAAAACAGCTAAGTACCTAGAAGAGCTCCCTGC
AAGTGTAAATATTAAGGATGACCTGTGCAAAATTATACCCACACCAGCACTAGTGGTAATTATTCTAAATTA

TTGCCAAAAAGTTTTTTTTAATCTGTCTTTCAAGTTTACAGAAAAGAAAGCAGTAAATGCATTGATGTCATT
TTATTATGTACATATATCATGTGCATTCAAGCTGTGTGACAAGATATATCAATATAAAAACAAGGTATATAC
TTTATTATTTTTTGAAAACAAGGATATTGTGATCAATTTTACCCTGTAAAACATATTTCTGTATTTATAGGT
CTTAAACATGATGAATTTTTTCTATTACAAGTTTATTTAAAACTGCTTTCTCAAGTCGTTATTGATACAGCA
AGTGAACCTGCTGCAGACAGAAGCAGAGGAAAGCCAAGAACAGCCTTTATTGGTGAAGAAAAGAATGAATGA
TTCTTTGTAGGCGCCATCAGCCACTTTTAGAAGCCATCAGCCAGTGTGTTGGGAAAAGAGGTTTGTCAAGTG
TTGGCCTATGGGAAGGTGGTCAATGAATGTTTTGATGAAATGAATGTTTTTGTATAATGGCCTTAAACTTTT
CTGGAAGTATTTCAAATAAATTACATTATTAAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:2

MVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPLSRVTSLANLIPPVKATPLKRFSQTLQRSIS
FRSESRPDILAPRPWSRNAAPSSTKRRDSKLWSETFDVCVNQMLTSKEIKRQEAIFELSQGEEDLIEDLKLA
KKAYHDPMLKLSIMTEQELNQIFGTLDSLIPLHEELLSQLRDVRKPDGSTEHVGPILVGWLPCLSSYDSYCS
NQVAAKALLDHKKQDHRVQDFLQRCLESPFSRKLDLWNFLDIPRSRLVKYPLLLREILRHTPNDNPDQQHLE
EAINIIQGIVAEINTKTGESECRYYKERLLYLEEGQKDSLIDSSRVLCCHGELKNNRGVKLHVFLFQEVLVI
TRAVTHNEQLCYQLYRQPIPVKDLLLEDLQDGEVRLGGSLRGAFSNNERIKNFFRVSFKNGSQSQTHSLQAN
DTFNKQQWLNCIRQAKETVLCAAGQAGVLDSEGSFLNPTTGSRELQGETKLEQMDQSDSESDCSMDTSEVSL
DCERMEQTDSSCGNSRHGESNV

SEQ ID NO:3

ATCTTTGAGCTTTCCCAAGGAGAAGAAGACTTGATAGAAGACTTGAAATTAGCAAAAAAGGCCTATCATGAC
CCCATGCTGAAACTCTCCATAATGACAGAACAAGAGTTGAATCAAATTTTTGGAACACTGGACTCTCTAATT
CCTCTACATGAAGAGCTCCTTAGTCAGCTTCGAGATGTTAGGAAGCCTGATGGCTCGACTGAACATGTTGGT
CCCATCCTCGTGGGCTGGCTCCCTTGCCTCAGCTCCTATGATAGCTACTGCAGCAATCAAGTAGCCGCCAAA
GCTCTGCTGGACCACAAAAAGCAAGATCACCGAGTCCAGGATTTCCTACAGCGATGTTTAGAATCCCCCTTT
AGCCGCAAACTAGATCTCTGGAATTTCCTCGATATTCCAAGAAGCCGCCTGGTAAAATACCCTCTGCTTCTC
CGAGAAATCTTGAGGCACACACCAAATGATAATCCAGATCAGCAGCACTTGGAAGAAGCTATAAATATCATT
CAGGGAATTGTGGCAGAAATCAACACCAAGACTGGTGAATCTGAATGCCGCTATTATAAAGAAGGCGGCTTC
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CACAATGAGCAGCTTTGCTACCAGCTGTACCGTCAGCCAATCCCCGTGAAAGACCTCCTGCTGGAAGACCTC
CAGGATGGAGAAGTGAGGCTGGGTGGCTCCCTGCGAGGGGCATTCAGCAACAATGAGAGAATTAAAAACTTC
TTCAGAGTCAGTTTCAAAAATGGATCCCAAAGTCAGACCCACTCGCTTACAAGCCAATGGACACTTTTCAAC
AAACAGCAGTGGCTTAACTGTATTCGTCAAGCCAAAGAAACAGTT

SEQ ID NO:4

IFELSQGEEDLIEDLKLAKKAYHDPMLKLSIMTEQELNQIFGTLDSLIPLHEELLSQLRDVRKPDGSTEHVG
PILVGWLPCLSSYDSYCSNQVAAKALLDHKKQDHRVQDFLQRCLESPFSRKLDLWNFLDIPRSRLVKYPLLL
REILRHTPNDNPDQQHLEEAINIIQGIVAEINTKTGESECRYYKEGGFFTWKKARKTPWIDSSRVLCCHGEL
KNNRGREMHVFLFQEVLVITRAVTHNEQLCYQLYRQPIPVKDLLLEDLQDGEVRLGGSLRGAFSNNERIKNF
FRVSFKNGSQSQTHSLTSQWTLFNKQQWLNCIRQAKETV

SEQ ID NO:5

GTGAGTTTTCCAGCCTGGAGAGGCCGAACCAGCGCGGGGGTCGAGGAGACCTGAGCCTGCCATACTGAGTCT
ATGGACAGTTCCACAGCAATGAATCAATGCAGCTGTAGAGGAATGGAAGAAAACAAGGAAAGGCCTAAACGG
CAGCGGCAAAACAACTTTCCCATGTTTCCCTCTCCTAAAGCCTGGAATTTCAGAGGGCGAAAACGGAAACAG
AGCACCCAAGATGAAGATGCTGTTAGCCTTTGCAGTCTCGACATAAGTGAGCCTAGTAATAAACGGGTCAAA
CCCCTTTCCCGAGCCACGTCGCTAGCAAACCTCATCCCGCCCGTGAAGGCCACGCCATTAAAGCGCTTCAGT
CAAACCCTGCAGCGCTCCATTAGCTTCCGCAGTGAGAGCCGCCCTGACATCCTCGCCCCCCGACCCTGGTCC
AGAAATGCCGCCCCCTCGAGCACGAAACGGAGAGATAGCAAGCTGTGGAGTGAGACCTTCGATGTGTGCGTC
AATCAGATGCTTACATCCAAGGAAATCAAACGTCAGGAGGCGATCTTTGAGCTTTCCCAAGGAGAAGAAGAC
TTGATAGAAGACTTGAAATTAGCAAAAAAGGCCTATCATGACCCCATGCTGAAACTCTCCATAATGACAGAA
CAAGAGTTGAATCAAATTTTTGGAACACTGGACTCTCTAATTCCTCTACATGAAGAGCTCCTTAGTCAGCTT
CGAGATGTTAGGAAGCCTGATGGCTCGACTGAACATGTTGGTCCCATCCTCGTGGGCTGGCTCCCTTGCCTC
AGCTCCTATGATAGCTACTGCAGCAATCAAGTAGCCGCCAAAGCTCTGCTGGACCACAAAAAGCAAGATCAC
CGAGTCCAGGATTTCCTACAGCGATGTTTAGAATCCCCCTTTAGCCGCAAACTAGATCTCTGGAATTTCCTC
GATATTCCAAGAAGCCGCCTGGTAAAATACCCTCTGCTTCTCCGAGAAATCTTGAGGCACACACCAAATGAT
AATCCAGATCAGCAGCACTTGGAAGAAGCTATAAATATCATTCAGGGAATTGTGGCAGAAATCAACACCAAG
ACTGGTGAATCTGAATGCCGCTATTATAAAGAGCGGCTTCTTTACTTGGAAGAAGGCCAGAAAGACTCCCTG
ATCGACAGCTCTCGAGTCTTGTGTTGTCATGGTGAACTGAAGAACAATCGGGGCGTGAAACTGCATGTTTTC
CTGTTCCAAGAAGTGCTTGTGATCACTCGAGCCGTCACCCACAATGAGCAGCTTTGCTACCAGCTGTACCGT
CAGCCAATCCCCGTGAAAGACCTCCTGCTGGAAGACCTCCAGGATGGAGAAGTGAGGCTGGGTGGCTCCCTG
CGAGGGGCATTCAGCAACAATGAGAGAATTAAAAACTTCTTCAGAGTCAGTTTCAAAAATGGATCCCAAAGT
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GAAACAGTTTTGTGTGCTGCCGGGCAAGCTGGGGTGCTTGACTCCGAGGGATCGTTCCTAAATCCCACCACC
GGGAGCAGAGAGCTACAGGGAGAAACAAAACTTGAGCAGATGGACCAATCGGACAGTGAGTCAGACTGTAGT
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CACGGTGAAAGTAACGTCTGACAGAAGCATGTGCACTTCGGGAAGCAGGCCTGCATCTTACCTGTACAGTAT
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GTCTCTCGTATCTGTACCTTTGTCCCTAGTACTGTAACTGCCAATCTGTCTGTGTAAGCTGGAATCTGTGGC
AACTATTACCCTGTGTTGTATTTCCCAAGTGTCTGGATGGATGGAGAGGTACTCAAACAAGTTACTTTCAGT
TGTCCTGCTGGATTTTAAAAAAATAGAAAAAGAATCTCAAAACTACTGTTTTACATAGATTGTTTGAAGAGT
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CCTTGTAAATAGGGCATGAGGAACTCATCTGTGTATTGGGATGGTATTAGAGAGAGAATCAGGAAAGACCAA
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TAATTTTGCAAAGGAGGATGCATTGTCTGAACTTTGCAACTTCATCCAGTGCAAGTTTGATGCAAGAATGTA
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GGGCTTAGGAAGGCCTGCCAGGATAACAAGAAGGCCCTGTATTCATTGTGTTTCATCTGCCTAGGCCTACTC
ATTATTTTAGAGAATGAATGAAGCAACAAGGAAGAGAGACCATGACTCTATCGATGACACTGTTTATAGAAA
CACAGGAGAGGAAGAATTTGGAATGAAAAGCACTTCGTCAGAACCTTCTGTGGGAGCCATTGAGAGAAAAGC
ATGGTCCAGTGCCTTCTGAGAAAGGCCAGAGCTTTGGGCTTTCCTGCTCTGCTTTTGGGTCGTCAATTTGCC
ATCTCTGGTTCTGTGCTATAATCAGAATTGTAATTATGTTCTCCAGAGGCCAATTTCATTAACTCTGATTAA
TTAGAATCAGCTAGCCAGATTAGTAACCTCTTTGTCCAGCCTTGATTTACAGTGCAGGGTAAAGTGCAGACC
TTAAAAACAGCTAAGTACCTAGAAGAGCTCCCTGCAAGTGTAAATATTAAGGATGACCTGTGCAAAATTATA
CCCACACCAGCACTAGTGGTAATTATTCTAAATTATTGCCAAAAAGTTTTTTTTAATCTGTCTTTCAAGTTT

ACAGAAAAGAAAGCAGTAAATGCATTGATGTCATTTTATTATGTACATATATCATGTGCATTCAAGCTGTGT
GACAAGATATATCAATATAAAAACAAGGTATATACTTTATTATTTTTTGAAAACAAGGATATTGTGATCAAT
TTTACCCTGTAAAACATATTTCTGTATTTATAGGTCTTAAACATGATGAATTTTTTCTATTACAAGTTTATT
TAAAACTGCTTTCTCAAGTCGTTATTGATACAGCAAGTGAACCTGCTGCAGACAGAAGCAGAGGAAAGCCAA
GAACAGCCTTTATTGGTGAAGAAAAGAATGAATGATTCTTTGTAGGCGCCATCAGCCACTTTTAGAAGCCAT
CAGCCAGTGTGTTGGGAAAAGAGGTTTGTCAAGTGTTGGCCTATGGGAAGGTGGTCAATGAATGTTTTGATG
AAATGAATGTTTTTGTATAATGGCCTTAAACTTTTCTGGAAGTATTTCAAATAAATTACATTATTAAGTCAA
AAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:6

MDSSTAMNQCSCRGMEENKERPKRQRQNNFPMFPSPKAWNFRGRKRKQSTQDEDAVSLCSLDISEPSNKRVK
PLSRATSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRPWSRNAAPSSTKRRDSKLWSETFDVCV
NQMLTSKEIKRQEAIFELSQGEEDLIEDLKLAKKAYHDPMLKLSIMTEQELNQIFGTLDSLIPLHEELLSQL
RDVRKPDGSTEHVGPILVGWLPCLSSYDSYCSNQVAAKALLDHKKQDHRVQDFLQRCLESPFSRKLDLWNFL
DIPRSRLVKYPLLLREILRHTPNDNPDQQHLEEAINIIQGIVAEINTKTGESECRYYKERLLYLEEGQKDSL
IDSSRVLCCHGELKNNRGVKLHVFLFQEVLVITRAVTHNEQLCYQLYRQPIPVKDLLLEDLQDGEVRLGGSL
RGAFSNNERIKNFFRVSFKNGSQSQTHSLQANDTFNKQQWLNCIRQAKETVLCAAGQAGVLDSEGSFLNPTT
GSRELQGETKLEQMDQSDSESDCSMDTSEVSLDCERMEQTDSSCGNSRHGESNV

Annex to the description

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: SmithKline Beecham plc

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SmithKline Beecham
(B) STREET: New Horizons Court, Great West Road
(C) CITY: Brentford
(D) STATE:
(E) COUNTRY: UK
(F) ZIP: TW8 9ET

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TAGAAGCCGG CTGTCGGTCT CCGTGTCGCC GCCGCCGCCC GGCATCGTGG AGCTGGGGCC     60
CCCTTTTGCC TGGGAGTTTT GTAGTCGCCT AGGGTCAGCG GTGACATCCC AAAGGGCAGG    120
CCCGGCAGCC GCCATGGTGG CCAAGGATTA CCCCTTCTAC CTCACGGTCA AGAGAGCGAA    180
CTGCAGCCTG GAGCTACCCC CGGCCAGCGG TCCGGCCAAG GACGCTGAGG AGCCTAGTAA    240
TAAACGGGTC AAACCCCTTT CCCGAGTCAC GTCGCTAGCA AACCTCATCC CGCCCGTGAA    300
GGCCACGCCA TTAAAGCGCT TCAGTCAAAC CCTGCAGCGC TCCATTAGCT TCCGCAGTGA    360
GAGCCGCCCT GACATCCTCG CCCCCCGACC CTGGTCCAGA AATGCCGCCC CCTCGAGCAC    420
GAAACGGAGA GATAGCAAGC TGTGGAGTGA GACCTTCGAT GTGTGCGTCA ATCAGATGCT    480
TACATCCAAG GAAATCAAAC GTCAGGAGGC GATCTTTGAG CTTTCCCAAG GAGAAGAAGA    540
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CTTGATAGAA GACTTGAAAT TAGCAAAAAA GGCCTATCAT GACCCCATGC TGAAACTCTC    600
CATAATGACA GAACAAGAGT TGAATCAAAT TTTTGGAACA CTGGACTCTC TAATTCCTCT    660
ACATGAAGAG CTCCTTAGTC AGCTTCGAGA TGTTAGGAAG CCTGATGGCT CGACTGAACA    720
TGTTGGTCCC ATCCTCGTGG GCTGGCTCCC TTGCCTCAGC TCCTATGATA GCTACTGCAG    780
CAATCAAGTA GCCGCCAAAG CTCTGCTGGA CCACAAAAAG CAAGATCACC GAGTCCAGGA    840
TTTCCTACAG CGATGTTTAG AATCCCCCTT TAGCCGCAAA CTAGATCTCT GGAATTTCCT    900
CGATATTCCA AGAAGCCGCC TGGTAAAATA CCCTCTGCTT CTCCGAGAAA TCTTGAGGCA    960
CACACCAAAT GATAATCCAG ATCAGCAGCA CTTGGAAGAA GCTATAAATA TCATTCAGGG   1020
AATTGTGGCA GAAATCAACA CCAAGACTGG TGAATCTGAA TGCCGCTATT ATAAAGAGCG   1080
GCTTCTTTAC TTGGAAGAAG GCCAGAAAGA CTCCCTGATC GACAGCTCTC GAGTCTTGTG   1140
TTGTCATGGT GAACTGAAGA ACAATCGGGG CGTGAAACTG CATGTTTTCC TGTTCCAAGA   1200
AGTGCTTGTG ATCACTCGAG CCGTCACCCA CAATGAGCAG CTTTGCTACC AGCTGTACCG   1260
TCAGCCAATC CCCGTGAAAG ACCTCCTGCT GGAAGACCTC CAGGATGGAG AAGTGAGGCT   1320
GGGTGGCTCC CTGCGAGGGG CATTCAGCAA CAATGAGAGA ATTAAAAACT TCTTCAGAGT   1380
CAGTTTCAAA AATGGATCCC AAAGTCAGAC CCACTCGCTA CAAGCCAATG ACACTTTCAA   1440
CAAACAGCAG TGGCTTAACT GTATTCGTCA AGCCAAAGAA ACAGTTTTGT GTGCTGCCGG   1500
GCAAGCTGGG GTGCTTGACT CCGAGGGATC GTTCCTAAAT CCCACCACCG GGAGCAGAGA   1560
GCTACAGGGA GAAACAAAAC TTGAGCAGAT GGACCAATCG GACAGTGAGT CAGACTGTAG   1620
TATGGACACG AGTGAGGTCA GCCTCGACTG TGAGCGCATG GAACAGACAG ACTCTTCCTG   1680
TGGAAACAGC AGGCACGGTG AAAGTAACGT CTGACAGAAG CATGTGCACT TCGGGAAGCA   1740
GGCCTGCATC TTACCTGTAC AGTATTTGCA TTCCACAGAT GGAACGGTTT GGAGAAGCAC   1800
TTTTTCATAC TTTTGTGAAA GTATACATGT TGGCCCAGTC TCTCGTATCT GTACCTTTGT   1860
CCCTAGTACT GTAACTGCCA ATCTGTCTGT GTAAGCTGGA ATCTGTGGCA ACTATTACCC   1920
TGTGTTGTAT TTCCCAAGTG TCTGGATGGA TGGAGAGGTA CTCAAACAAG TTACTTTCAG   1980
TTGTCCTGCT GGATTTTAAA AAAATAGAAA AAGAATCTCA AAACTACTGT TTTACATAGA   2040
TTGTTTGAAG AGTCCTTCCT CTTGTGCTTC TGTACCACTT TCCCAGCTCT TAGATGTGGT   2100
AGCTAAAGGC ACGGAATTTA GACGGCCTTG TAAATAGGGC ATGAGGAACT CATCTGTGTA   2160
TTGGGATGGT ATTAGAGAGA GAATCAGGAA AGACCAACTC ATGAAGTGAA CTTGGTTTGA   2220
TCTTACTCAA CTAGAAAGCT TGAAAACATC CCTGGGGATT CTGAAGGCTT AATTTTGCAA   2280
AGGAGGATGC ATTGTCTGAA CTTTGCAACT TCATCCAGTG CAAGTTTGAT GCAAGAATGT   2340
ATTAGGACAT AAAATAGAGG CTGACCTTAA AAGGGCCAGG ACAGAAGCGG CTGCCAGCTC   2400
TGAATCTTTA ACTGAAATGC ACATGGCACC AGGAGGTGTC TCTCATAGTT GGTTGCTAGC   2460
CTAAAACATC AGAATAGAAC CCAAAGGGCT TAGGAAGGCC TGCCAGGATA ACAAGAAGGC   2520
CCTGTATTCA TTGTGTTTCA TCTGCCTAGG CCTACTCATT ATTTTAGAGA ATGAATGAAG   2580
CAACAAGGAA GAGAGACCAT GACTCTATCG ATGACACTGT TTATAGAAAC ACAGGAGAGG   2640
AAGAATTTGG AATGAAAAGC ACTTCGTCAG AACCTTCTGT GGGAGCCATT GAGAGAAAAG   2700
CATGGTCCAG TGCCTTCTGA GAAAGGCCAG AGCTTTGGGC TTTCCTGCTC TGCTTTTGGG   2760
TCGTCAATTT GCCATCTCTG GTTCTGTGCT ATAATCAGAA TTGTAATTAT GTTCTCCAGA   2820
GGCCAATTTC ATTAACTCTG ATTAATTAGA ATCAGCTAGC CAGATTAGTA ACCTCTTTGT   2880
CCAGCCTTGA TTTACAGTGC AGGGTAAAGT GCAGACCTTA AAAACAGCTA AGTACCTAGA   2940
AGAGCTCCCT GCAAGTGTAA ATATTAAGGA TGACCTGTGC AAAATTATAC CCACACCAGC   3000
ACTAGTGGTA ATTATTCTAA ATTATTGCCA AAAAGTTTTT TTTAATCTGT CTTTCAAGTT   3060
TACAGAAAAG AAAGCAGTAA ATGCATTGAT GTCATTTTAT TATGTACATA TATCATGTGC   3120
ATTCAAGCTG TGTGACAAGA TATATCAATA TAAAAACAAG GTATATACTT TATTATTTTT   3180
TGAAAACAAG GATATTGTGA TCAATTTTAC CCTGTAAAAC ATATTTCTGT ATTTATAGGT   3240
CTTAAACATG ATGAATTTTT TCTATTACAA GTTTATTTAA AACTGCTTTC TCAAGTCGTT   3300
ATTGATACAG CAAGTGAACC TGCTGCAGAC AGAAGCAGAG GAAAGCCAAG AACAGCCTTT   3360
ATTGGTGAAG AAAAGAATGA ATGATTCTTT GTAGGCGCCA TCAGCCACTT TTAGAAGCCA   3420
TCAGCCAGTG TGTTGGGAAA AGAGGTTTGT CAAGTGTTGG CCTATGGGAA GGTGGTCAAT   3480
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GAATGTTTTG ATGAAATGAA TGTTTTTGTA TAATGGCCTT AAACTTTTCT GGAAGTATTT 3540
CAAATAAATT ACATTATTAA GTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 3592

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 526 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Ala Lys Asp Tyr Pro Phe Tyr Leu Thr Val Lys Arg Ala Asn
1 5 10 15
Cys Ser Leu Glu Leu Pro Pro Ala Ser Gly Pro Ala Lys Asp Ala Glu
20 25 30
Glu Pro Ser Asn Lys Arg Val Lys Pro Leu Ser Arg Val Thr Ser Leu
35 40 45
Ala Asn Leu Ile Pro Pro Val Lys Ala Thr Pro Leu Lys Arg Phe Ser
50 55 60
Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg Ser Glu Ser Arg Pro Asp
65 70 75 80
Ile Leu Ala Pro Arg Pro Trp Ser Arg Asn Ala Ala Pro Ser Ser Thr
85 90 95
Lys Arg Arg Asp Ser Lys Leu Trp Ser Glu Thr Phe Asp Val Cys Val
100 105 110
Asn Gln Met Leu Thr Ser Lys Glu Ile Lys Arg Gln Glu Ala Ile Phe
115 120 125
Glu Leu Ser Gln Gly Glu Glu Asp Leu Ile Glu Asp Leu Lys Leu Ala
130 135 140
Lys Lys Ala Tyr His Asp Pro Met Leu Lys Leu Ser Ile Met Thr Glu
145 150 155 160
Gln Glu Leu Asn Gln Ile Phe Gly Thr Leu Asp Ser Leu Ile Pro Leu
165 170 175
His Glu Glu Leu Leu Ser Gln Leu Arg Asp Val Arg Lys Pro Asp Gly
180 185 190
Ser Thr Glu His Val Gly Pro Ile Leu Val Gly Trp Leu Pro Cys Leu
195 200 205
Ser Ser Tyr Asp Ser Tyr Cys Ser Asn Gln Val Ala Ala Lys Ala Leu
210 215 220
Leu Asp His Lys Lys Gln Asp His Arg Val Gln Asp Phe Leu Gln Arg
225 230 235 240
Cys Leu Glu Ser Pro Phe Ser Arg Lys Leu Asp Leu Trp Asn Phe Leu
245 250 255
Asp Ile Pro Arg Ser Arg Leu Val Lys Tyr Pro Leu Leu Leu Arg Glu
260 265 270

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Ile Leu Arg His Thr Pro Asn Asp Asn Pro Asp Gln Gln His Leu Glu
        275                 280                 285
Glu Ala Ile Asn Ile Ile Gln Gly Ile Val Ala Glu Ile Asn Thr Lys
    290                 295                 300
Thr Gly Glu Ser Glu Cys Arg Tyr Tyr Lys Glu Arg Leu Leu Tyr Leu
305                 310                 315                 320
Glu Glu Gly Gln Lys Asp Ser Leu Ile Asp Ser Ser Arg Val Leu Cys
                325                 330                 335
Cys His Gly Glu Leu Lys Asn Asn Arg Gly Val Lys Leu His Val Phe
            340                 345                 350
Leu Phe Gln Glu Val Leu Val Ile Thr Arg Ala Val Thr His Asn Glu
        355                 360                 365
Gln Leu Cys Tyr Gln Leu Tyr Arg Gln Pro Ile Pro Val Lys Asp Leu
    370                 375                 380
Leu Leu Glu Asp Leu Gln Asp Gly Glu Val Arg Leu Gly Gly Ser Leu
385                 390                 395                 400
Arg Gly Ala Phe Ser Asn Asn Glu Arg Ile Lys Asn Phe Phe Arg Val
                405                 410                 415
Ser Phe Lys Asn Gly Ser Gln Ser Gln Thr His Ser Leu Gln Ala Asn
            420                 425                 430
Asp Thr Phe Asn Lys Gln Gln Trp Leu Asn Cys Ile Arg Gln Ala Lys
        435                 440                 445
Glu Thr Val Leu Cys Ala Ala Gly Gln Ala Gly Val Leu Asp Ser Glu
    450                 455                 460
Gly Ser Phe Leu Asn Pro Thr Thr Gly Ser Arg Glu Leu Gln Gly Glu
465                 470                 475                 480
Thr Lys Leu Glu Gln Met Asp Gln Ser Asp Ser Glu Ser Asp Cys Ser
                485                 490                 495
Met Asp Thr Ser Glu Val Ser Leu Asp Cys Glu Arg Met Glu Gln Thr
            500                 505                 510
Asp Ser Ser Cys Gly Asn Ser Arg His Gly Glu Ser Asn Val
        515                 520                 525
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATCTTTGAGC TTTCCCAAGG AGAAGAAGAC TTGATAGAAG ACTTGAAATT AGCAAAAAAG     60
GCCTATCATG ACCCCATGCT GAAACTCTCC ATAATGACAG AACAAGAGTT GAATCAAATT    120
TTTGGAACAC TGGACTCTCT AATTCCTCTA CATGAAGAGC TCCTTAGTCA GCTTCGAGAT    180
GTTAGGAAGC CTGATGGCTC GACTGAACAT GTTGGTCCCA TCCTCGTGGG CTGGCTCCCT    240
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TGCCTCAGCT CCTATGATAG CTACTGCAGC AATCAAGTAG CCGCCAAAGC TCTGCTGGAC    300
CACAAAAAGC AAGATCACCG AGTCCAGGAT TTCCTACAGC GATGTTTAGA ATCCCCCTTT    360
AGCCGCAAAC TAGATCTCTG GAATTTCCTC GATATTCCAA GAAGCCGCCT GGTAAAATAC    420
CCTCTGCTTC TCCGAGAAAT CTTGAGGCAC ACACCAAATG ATAATCCAGA TCAGCAGCAC    480
TTGGAAGAAG CTATAAATAT CATTCAGGGA ATTGTGGCAG AAATCAACAC CAAGACTGGT    540
GAATCTGAAT GCCGCTATTA TAAAGAAGGC GGCTTCTTTA CTTGGAAGAA GGCCAGAAAG    600
ACTCCCTGGA TCGACAGCTC TCGAGTCTTG TGTTGTCATG GTGAACTGAA GAACAATCGG    660
GGCAGAGAAA TGCATGTTTT CCTGTTCCAA GAAGTGCTTG TGATCACTCG AGCCGTCACC    720
CACAATGAGC AGCTTTGCTA CCAGCTGTAC CGTCAGCCAA TCCCCGTGAA AGACCTCCTG    780
CTGGAAGACC TCCAGGATGG AGAAGTGAGG CTGGGTGGCT CCCTGCGAGG GGCATTCAGC    840
AACAATGAGA GAATTAAAAA CTTCTTCAGA GTCAGTTTCA AAAATGGATC CCAAAGTCAG    900
ACCCACTCGC TTACAAGCCA ATGGACACTT TTCAACAAAC AGCAGTGGCT TAACTGTATT    960
CGTCAAGCCA AAGAAACAGT T                                              981
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Ile Phe Glu Leu Ser Gln Gly Glu Glu Asp Leu Ile Glu Asp Leu Lys
 1               5                  10                  15
Leu Ala Lys Lys Ala Tyr His Asp Pro Met Leu Lys Leu Ser Ile Met
            20                  25                  30
Thr Glu Gln Glu Leu Asn Gln Ile Phe Gly Thr Leu Asp Ser Leu Ile
        35                  40                  45
Pro Leu His Glu Glu Leu Leu Ser Gln Leu Arg Asp Val Arg Lys Pro
    50                  55                  60
Asp Gly Ser Thr Glu His Val Gly Pro Ile Leu Val Gly Trp Leu Pro
65                  70                  75                  80
Cys Leu Ser Ser Tyr Asp Ser Tyr Cys Ser Asn Gln Val Ala Ala Lys
                85                  90                  95
Ala Leu Leu Asp His Lys Lys Gln Asp His Arg Val Gln Asp Phe Leu
            100                 105                 110
Gln Arg Cys Leu Glu Ser Pro Phe Ser Arg Lys Leu Asp Leu Trp Asn
        115                 120                 125
Phe Leu Asp Ile Pro Arg Ser Arg Leu Val Lys Tyr Pro Leu Leu Leu
    130                 135                 140
Arg Glu Ile Leu Arg His Thr Pro Asn Asp Asn Pro Asp Gln Gln His
145                 150                 155                 160
Leu Glu Glu Ala Ile Asn Ile Ile Gln Gly Ile Val Ala Glu Ile Asn
                165                 170                 175
Thr Lys Thr Gly Glu Ser Glu Cys Arg Tyr Tyr Lys Glu Gly Gly Phe
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            180                 185                 190
Phe Thr Trp Lys Lys Ala Arg Lys Thr Pro Trp Ile Asp Ser Ser Arg
        195                 200                 205
Val Leu Cys Cys His Gly Glu Leu Lys Asn Asn Arg Gly Arg Glu Met
    210                 215                 220
His Val Phe Leu Phe Gln Glu Val Leu Val Ile Thr Arg Ala Val Thr
225                 230                 235                 240
His Asn Glu Gln Leu Cys Tyr Gln Leu Tyr Arg Gln Pro Ile Pro Val
                245                 250                 255
Lys Asp Leu Leu Leu Glu Asp Leu Gln Asp Gly Glu Val Arg Leu Gly
            260                 265                 270
Gly Ser Leu Arg Gly Ala Phe Ser Asn Asn Glu Arg Ile Lys Asn Phe
        275                 280                 285
Phe Arg Val Ser Phe Lys Asn Gly Ser Gln Ser Gln Thr His Ser Leu
    290                 295                 300
Thr Ser Gln Trp Thr Leu Phe Asn Lys Gln Gln Trp Leu Asn Cys Ile
305                 310                 315                 320
Arg Gln Ala Lys Glu Thr Val
                325
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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3627 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GTGAGTTTTC CAGCCTGGAG AGGCCGAACC AGCGCGGGGG TCGAGGAGAC CTGAGCCTGC     60
CATACTGAGT CTATGGACAG TTCCACAGCA ATGAATCAAT GCAGCTGTAG AGGAATGGAA    120
GAAAACAAGG AAAGGCCTAA ACGGCAGCGG CAAAACAACT TTCCCATGTT TCCCTCTCCT    180
AAAGCCTGGA ATTTCAGAGG GCGAAAACGG AAACAGAGCA CCCAAGATGA AGATGCTGTT    240
AGCCTTTGCA GTCTCGACAT AAGTGAGCCT AGTAATAAAC GGGTCAAACC CCTTTCCCGA    300
GCCACGTCGC TAGCAAACCT CATCCCGCCC GTGAAGGCCA CGCCATTAAA GCGCTTCAGT    360
CAAACCCTGC AGCGCTCCAT TAGCTTCCGC AGTGAGAGCC GCCCTGACAT CCTCGCCCCC    420
CGACCCTGGT CCAGAAATGC CGCCCCCTCG AGCACGAAAC GGAGAGATAG CAAGCTGTGG    480
AGTGAGACCT TCGATGTGTG CGTCAATCAG ATGCTTACAT CCAAGGAAAT CAAACGTCAG    540
GAGGCGATCT TTGAGCTTTC CCAAGGAGAA GAAGACTTGA TAGAAGACTT GAAATTAGCA    600
AAAAAGGCCT ATCATGACCC CATGCTGAAA CTCTCCATAA TGACAGAACA AGAGTTGAAT    660
CAAATTTTTG GAACACTGGA CTCTCTAATT CCTCTACATG AAGAGCTCCT TAGTCAGCTT    720
CGAGATGTTA GGAAGCCTGA TGGCTCGACT GAACATGTTG GTCCCATCCT CGTGGGCTGG    780
CTCCCTTGCC TCAGCTCCTA TGATAGCTAC TGCAGCAATC AAGTAGCCGC CAAAGCTCTG    840
CTGGACCACA AAAAGCAAGA TCACCGAGTC CAGGATTTCC TACAGCGATG TTTAGAATCC    900
CCCTTTAGCC GCAAACTAGA TCTCTGGAAT TTCCTCGATA TTCCAAGAAG CCGCCTGGTA    960
AAATACCCTC TGCTTCTCCG AGAAATCTTG AGGCACACAC CAAATGATAA TCCAGATCAG   1020
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CAGCACTTGG AAGAAGCTAT AAATATCATT CAGGGAATTG TGGCAGAAAT CAACACCAAG 1080
ACTGGTGAAT CTGAATGCCG CTATTATAAA GAGCGGCTTC TTTACTTGGA AGAAGGCCAG 1140
AAAGACTCCC TGATCGACAG CTCTCGAGTC TTGTGTTGTC ATGGTGAACT GAAGAACAAT 1200
CGGGGCGTGA AACTGCATGT TTTCCTGTTC CAAGAAGTGC TTGTGATCAC TCGAGCCGTC 1260
ACCCACAATG AGCAGCTTTG CTACCAGCTG TACCGTCAGC CAATCCCCGT GAAAGACCTC 1320
CTGCTGGAAG ACCTCCAGGA TGGAGAAGTG AGGCTGGGTG GCTCCCTGCG AGGGGCATTC 1380
AGCAACAATG AGAGAATTAA AAACTTCTTC AGAGTCAGTT TCAAAAATGG ATCCCAAAGT 1440
CAGACCCACT CGCTACAAGC CAATGACACT TTCAACAAAC AGCAGTGGCT TAACTGTATT 1500
CGTCAAGCCA AAGAAACAGT TTTGTGTGCT GCCGGGCAAG CTGGGGTGCT TGACTCCGAG 1560
GGATCGTTCC TAAATCCCAC CACCGGGAGC AGAGAGCTAC AGGGAGAAAC AAAACTTGAG 1620
CAGATGGACC AATCGGACAG TGAGTCAGAC TGTAGTATGG ACACGAGTGA GGTCAGCCTC 1680
GACTGTGAGC GCATGGAACA GACAGACTCT TCCTGTGGAA ACAGCAGGCA CGGTGAAAGT 1740
AACGTCTGAC AGAAGCATGT GCACTTCGGG AAGCAGGCCT GCATCTTACC TGTACAGTAT 1800
TTGCATTCCA CAGATGGAAC GGTTTGGAGA AGCACTTTTT CATACTTTTG TGAAAGTATA 1860
CATGTTGGCC CAGTCTCTCG TATCTGTACC TTTGTCCCTA GTACTGTAAC TGCCAATCTG 1920
TCTGTGTAAG CTGGAATCTG TGGCAACTAT TACCCTGTGT TGTATTTCCC AAGTGTCTGG 1980
ATGGATGGAG AGGTACTCAA ACAAGTTACT TTCAGTTGTC CTGCTGGATT TTAAAAAAAT 2040
AGAAAAAGAA TCTCAAAACT ACTGTTTTAC ATAGATTGTT TGAAGAGTCC TTCCTCTTGT 2100
GCTTCTGTAC CACTTTCCCA GCTCTTAGAT GTGGTAGCTA AAGGCACGGA ATTTAGACGG 2160
CCTTGTAAAT AGGGCATGAG GAACTCATCT GTGTATTGGG ATGGTATTAG AGAGAGAATC 2220
AGGAAAGACC AACTCATGAA GTGAACTTGG TTTGATCTTA CTCAACTAGA AAGCTTGAAA 2280
ACATCCCTGG GGATTCTGAA GGCTTAATTT TGCAAAGGAG GATGCATTGT CTGAACTTTG 2340
CAACTTCATC CAGTGCAAGT TTGATGCAAG AATGTATTAG GACATAAAAT AGAGGCTGAC 2400
CTTAAAAGGG CCAGGACAGA AGCGGCTGCC AGCTCTGAAT CTTTAACTGA AATGCACATG 2460
GCACCAGGAG GTGTCTCTCA TAGTTGGTTG CTAGCCTAAA ACATCAGAAT AGAACCCAAA 2520
GGGCTTAGGA AGGCCTGCCA GGATAACAAG AAGGCCCTGT ATTCATTGTG TTTCATCTGC 2580
CTAGGCCTAC TCATTATTTT AGAGAATGAA TGAAGCAACA AGGAAGAGAG ACCATGACTC 2640
TATCGATGAC ACTGTTTATA GAAACACAGG AGAGGAAGAA TTTGGAATGA AAAGCACTTC 2700
GTCAGAACCT TCTGTGGGAG CCATTGAGAG AAAAGCATGG TCCAGTGCCT TCTGAGAAAG 2760
GCCAGAGCTT TGGGCTTTCC TGCTCTGCTT TTGGGTCGTC AATTTGCCAT CTCTGGTTCT 2820
GTGCTATAAT CAGAATTGTA ATTATGTTCT CCAGAGGCCA ATTTCATTAA CTCTGATTAA 2880
TTAGAATCAG CTAGCCAGAT TAGTAACCTC TTTGTCCAGC CTTGATTTAC AGTGCAGGGT 2940
AAAGTGCAGA CCTTAAAAAC AGCTAAGTAC CTAGAAGAGC TCCCTGCAAG TGTAAATATT 3000
AAGGATGACC TGTGCAAAAT TATACCCACA CCAGCACTAG TGGTAATTAT TCTAAATTAT 3060
TGCCAAAAAG TTTTTTTTAA TCTGTCTTTC AAGTTTACAG AAAAGAAAGC AGTAAATGCA 3120
TTGATGTCAT TTTATTATGT ACATATATCA TGTGCATTCA AGCTGTGTGA CAAGATATAT 3180
CAATATAAAA ACAAGGTATA TACTTTATTA TTTTTTGAAA ACAAGGATAT TGTGATCAAT 3240
TTTACCCTGT AAAACATATT TCTGTATTTA TAGGTCTTAA ACATGATGAA TTTTTTCTAT 3300
TACAAGTTTA TTTAAAACTG CTTTCTCAAG TCGTTATTGA TACAGCAAGT GAACCTGCTG 3360
CAGACAGAAG CAGAGGAAAG CCAAGAACAG CCTTTATTGG TGAAGAAAAG AATGAATGAT 3420
TCTTTGTAGG CGCCATCAGC CACTTTTAGA AGCCATCAGC CAGTGTGTTG GGAAAAGAGG 3480
TTTGTCAAGT GTTGGCCTAT GGGAAGGTGG TCAATGAATG TTTTGATGAA ATGAATGTTT 3540
TTGTATAATG GCCTTAAACT TTTCTGGAAG TATTTCAAAT AAATTACATT ATTAAGTCAA 3600
AAAAAAAAAA AAAAAAAAAA AAAAAAA 3627

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 558 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Asp Ser Ser Thr Ala Met Asn Gln Cys Ser Cys Arg Gly Met Glu
 1               5                  10                  15
Glu Asn Lys Glu Arg Pro Lys Arg Gln Arg Gln Asn Asn Phe Pro Met
            20                  25                  30
Phe Pro Ser Pro Lys Ala Trp Asn Phe Arg Gly Arg Lys Arg Lys Gln
        35                  40                  45
Ser Thr Gln Asp Glu Asp Ala Val Ser Leu Cys Ser Leu Asp Ile Ser
    50                  55                  60
Glu Pro Ser Asn Lys Arg Val Lys Pro Leu Ser Arg Ala Thr Ser Leu
65                  70                  75                  80
Ala Asn Leu Ile Pro Pro Val Lys Ala Thr Pro Leu Lys Arg Phe Ser
                85                  90                  95
Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg Ser Glu Ser Arg Pro Asp
            100                 105                 110
Ile Leu Ala Pro Arg Pro Trp Ser Arg Asn Ala Ala Pro Ser Ser Thr
        115                 120                 125
Lys Arg Arg Asp Ser Lys Leu Trp Ser Glu Thr Phe Asp Val Cys Val
    130                 135                 140
Asn Gln Met Leu Thr Ser Lys Glu Ile Lys Arg Gln Glu Ala Ile Phe
145                 150                 155                 160
Glu Leu Ser Gln Gly Glu Glu Asp Leu Ile Glu Asp Leu Lys Leu Ala
                165                 170                 175
Lys Lys Ala Tyr His Asp Pro Met Leu Lys Leu Ser Ile Met Thr Glu
            180                 185                 190
Gln Glu Leu Asn Gln Ile Phe Gly Thr Leu Asp Ser Leu Ile Pro Leu
        195                 200                 205
His Glu Glu Leu Leu Ser Gln Leu Arg Asp Val Arg Lys Pro Asp Gly
    210                 215                 220
Ser Thr Glu His Val Gly Pro Ile Leu Val Gly Trp Leu Pro Cys Leu
225                 230                 235                 240
Ser Ser Tyr Asp Ser Tyr Cys Ser Asn Gln Val Ala Ala Lys Ala Leu
                245                 250                 255
Leu Asp His Lys Lys Gln Asp His Arg Val Gln Asp Phe Leu Gln Arg
            260                 265                 270
Cys Leu Glu Ser Pro Phe Ser Arg Lys Leu Asp Leu Trp Asn Phe Leu
        275                 280                 285
Asp Ile Pro Arg Ser Arg Leu Val Lys Tyr Pro Leu Leu Leu Arg Glu
    290                 295                 300
Ile Leu Arg His Thr Pro Asn Asp Asn Pro Asp Gln Gln His Leu Glu
305                 310                 315                 320
Glu Ala Ile Asn Ile Ile Gln Gly Ile Val Ala Glu Ile Asn Thr Lys
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                    325                 330                 335
Thr Gly Glu Ser Glu Cys Arg Tyr Tyr Lys Glu Arg Leu Leu Tyr Leu
            340                 345                 350
Glu Glu Gly Gln Lys Asp Ser Leu Ile Asp Ser Ser Arg Val Leu Cys
        355                 360                 365
Cys His Gly Glu Leu Lys Asn Asn Arg Gly Val Lys Leu His Val Phe
    370                 375                 380
Leu Phe Gln Glu Val Leu Val Ile Thr Arg Ala Val Thr His Asn Glu
385                 390                 395                 400
Gln Leu Cys Tyr Gln Leu Tyr Arg Gln Pro Ile Pro Val Lys Asp Leu
                405                 410                 415
Leu Leu Glu Asp Leu Gln Asp Gly Glu Val Arg Leu Gly Gly Ser Leu
            420                 425                 430
Arg Gly Ala Phe Ser Asn Asn Glu Arg Ile Lys Asn Phe Phe Arg Val
        435                 440                 445
Ser Phe Lys Asn Gly Ser Gln Ser Gln Thr His Ser Leu Gln Ala Asn
    450                 455                 460
Asp Thr Phe Asn Lys Gln Gln Trp Leu Asn Cys Ile Arg Gln Ala Lys
465                 470                 475                 480
Glu Thr Val Leu Cys Ala Ala Gly Gln Ala Gly Val Leu Asp Ser Glu
                485                 490                 495
Gly Ser Phe Leu Asn Pro Thr Thr Gly Ser Arg Glu Leu Gln Gly Glu
            500                 505                 510
Thr Lys Leu Glu Gln Met Asp Gln Ser Asp Ser Glu Ser Asp Cys Ser
        515                 520                 525
Met Asp Thr Ser Glu Val Ser Leu Asp Cys Glu Arg Met Glu Gln Thr
    530                 535                 540
Asp Ser Ser Cys Gly Asn Ser Arg His Gly Glu Ser Asn Val
545                 550                 555
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Claims

1. An isolated polypeptide comprising an amino acid sequence which has at least 70% identity to the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:6 over the entire length of of SEQ ID NO:2 or SEQ ID NO:6.

2. An isolated polypeptide as claimed in claim 1 in which the amino acid sequence has at least 95% identity.

3. The polypeptide as claimed in claim 1 comprising the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:6.

4. The isolated polypeptide of SEQ ID NO:2 or SEQ ID NO:6.

5. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide that has at least 70% identity to the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:6, over the entire length of SEQ ID NO:2 or SEQ ID NO:6; or a nucleotide sequence complementary to said isolated polynucleotide.

6. An isolated polynucleotide comprising a nucleotide sequence that has at least 70% identity to a nucleotide sequence encoding a polypeptide of SEQ ID NO:2 or SEQ ID NO:6, over the entire coding region; or a nucleotide sequence complementary to said isolated polynucleotide.

7. An isolated polynucleotide which comprises a nucleotide sequence which has at least 70% identity to that of SEQ

ID NO:1 or SEQ ID NO:5 over the entire length of SEQ ID NO:1 or SEQ ID NO:5 ; or a nucleotide sequence complementary to said isolated polynucleotide.

8. The isolated polynucleotide as claimed in any one of claims 5 to 7 in which the identity is at least 95%.

9. An isolated polynucleotide selected from:

(a) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO:2;
(b) the polynucleotide of SEQ ID NO:1 ; and
(c) a polynucleotide obtainable by screening an appropriate library under stringent hybridization conditions with a labeled probe having the sequence of SEQ ID NO:1 or a fragment thereof; or a nucleotide sequence complementary to said isolated polynucleotide,
(d) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO:6;
(e) the polynucleotide of SEQ ID NO:5; and
(f) a polynucleotide obtainable by screening an appropriate library under stringent hybridization conditions with a labeled probe having the sequence of SEQ ID NO:5 or a fragment thereof; or a nucleotide sequence complementary to said isolated polynucleotide

10. An expression system comprising a polynucleotide capable of producing a polypeptide of claim 1 when said expression system is present in a compatible host cell.

11. A host cell comprising the expression system of claim 15 or a membrane thereof expressing the polypeptide of claim 1.

12. A process for producing a polypeptide of claim 1 comprising culturing a host cell of claim 11 under conditions sufficient for the production of said polypeptide and recovering the polypeptide from the culture medium.

13. An antibody immunospecific for the polypeptide of claim 1.

14. A method for screening to identify compounds which stimulate or which inhibit the function of the polypeptide of claim 1 which comprises a method selected from the group consisting of:

(a) measuring the binding of a candidate compound to the polypeptide (or to the cells or membranes bearing the polypeptide) or a fusion protein thereof by means of a label directly or indirectly associated with the candidate compound;
(b) measuring the binding of a candidate compound to the polypeptide (or to the cells or membranes bearing the polypeptide) or a fusion protein thereof in the presense of a labeled competitior;
(c) testing whether the candidate compound results in a signal generated by activation or inhbition of the polypeptide, using detection systems appropriate to the cells or cell membranes bearing the polypeptide;
(d) mixing a candidate compound with a solution containing a polypeptide of claim 1, to form a mixture, measuring activity of the polypeptide in the mixture, and comparing the activity of the mixture to a standard; or
(e) detecting the effect of a candidate compound on the production of mRNA encoding said polypeptide and said polypeptide in cells, using for instance, an ELISA assay.

15. An agonist or antagonist to the polypeptide of claims 1 to 4.

16. A compound which is:

(a) an agonist or antagonist to the polypeptide of claims 1 to 4;
(b) isolated polynucleotide of claims 5 to 9; or
(c) a nucleic acid molecule that modulates the expression of the nucleotide sequence encoding the polypeptide of claim 1;

for use in therapy.

17. A process for diagnosing a disease or a susceptibility to a disease in a subject related to expression or activity of the polypeptide of claim 1 in a subject comprising:

(a) determining the presence or absence of a mutation in the nucleotide sequence encoding said polypeptide in the genome of said subject; and/or
(b) analyzing for the presence or amount of said polypeptide expression in a sample derived from said subject.

18. An isolated polynucleotide selected form the group consisting of:

(a) an isolated polynucleotide comprising a nucleotide sequence which has at least 70% identity to SEQ ID NO:3 over the entire length of SEQ ID NO:3;
(b) an isolated polynucleotide comprising the polynucleotide of SEQ ID NO:3;
(c) the polynucleotide of SEQ ID NO:3; or
(d) an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide which has at least 70% identity to the amino acid sequence of SEQ ID NO:4, over the entire length of SEQ ID NO:4.

19. A polypeptide selected from the group consisting of:

(a) a polypeptide which comprises an amino acid sequence which has at least 70% identity to that of SEQ ID NO:4 over the entire length of SEQ ID NO:4;
(b) a polypeptide in which the amino acid sequence has at least 70% identity to the amino acid sequence of SEQ ID NO:4 over the entire length of SEQ ID NO:4;
(c) a polypeptide which comprises the amino acid of SEQ ID NO:4;
(d) a polypeptide which is the polypeptide of SEQ ID NO:4; or
(e) a polypeptide which is encoded by a polynucleotide comprising the sequence contained in SEQ ID NO:3.

(19) Europäisches Patentamt
European Patent Office
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(11) EP 0 881 291 A3

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(54) CBS2 polypeptides, members of the guanine exchange factor family

(57) CSB2 polypeptides and polynucleotides and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing CSB2 polypeptides and polynucleotides in therapy, and diagnostic assays for such.

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European Patent Office

PARTIAL EUROPEAN SEARCH REPORT

which under Rule 45 of the European Patent Convention shall be considered, for the purposes of subsequent proceedings, as the European search report

Application Number EP 98 30 3990

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
X,D	ANDREW M-L ET AL: "Isolation of a novel oncogene, NET1, from neuroepitheliuma cells by expression cDNA cloning" ONCOGENE, vol. 12, 1996, pages 1259-1266, XP002098930 * page 1260; figure 1 *	18,19	C12N15/12 A61K38/17 C12Q1/68 C07K14/47 G01N33/68 C07K16/18
A	---	1-12,16	
A	HILLIER ET AL: "WashU-Merck EST project 1997" EMBL DATABASE ENTRY HSAA3078, ACCESSION NUMBER AA403078,1 May 1997, XP002098931 * abstract *	7-9	
A	--- L. HILLIER ET AL: "The WashU-Merck EST project" EMBL DATABASE ENTRY HSA01235, ACCESSION NUMBER AA001235,20 July 1996, XP002098932 * abstract *	7-9	
	--- -/--		TECHNICAL FIELDS SEARCHED (Int.Cl.6) C07K

INCOMPLETE SEARCH

The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.

Claims searched completely :

Claims searched incompletely :

Claims not searched :

Reason for the limitation of the search:

see sheet C

Place of search	Date of completion of the search	Examiner
THE HAGUE	8 April 1999	Le Cornec, N

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
P : intermediate document

T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons

& : member of the same patent family, corresponding document

EPO FORM 1503 03.82 (P04C07)

European Patent Office

INCOMPLETE SEARCH SHEET C

Application Number
EP 98 30 3990

Although claim 17 (as far as it concerns an in vivo method) is directed to a diagnostic method practised on the human/animal body (Article 52(4) EPC), the search has been carried out and based on the alleged effects of the compound/composition.

Claim(s) searched completely:
1-14,17-19

Claim(s) searched incompletely:
16

Claim(s) not searched:
15

Reason for the limitation of the search:

A meaningful search for claims 15 and 16 partially has not been possible because neither an antagonist nor an agonist of the polypeptide defined by sequences ID no. 2 and 6 nor a nucleic acid molecule that modulates the expression of the nucleotide sequence encoding the polypeptide defined by the sequences ID no. 2 and 6 has been characterized.

European Patent Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 98 30 3990

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
A	M.D. ADAMS ET AL: "EST56928 infant brain Homo sapiens cDNA 5' end" EMBL DATABASE ENTRY HSZZ55075, ACCESSION NUMBER AA349948,18 April 1997, XP002098933 * abstract * ---	7-9,18	
A	M.D. ADAMS ET AL: "Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence " EMBL DATABASE ENTRY HSZZ66205, ACCESSION NUMBER AA361004,18 April 1997, XP002098934 * abstract * ---	7-9	
A	L. HILLIER ET AL: "The WashU-Merck EST project" EMBL DATABASE ENTRY HSAA14633, ACCESSION NUMBER AA195613,24 January 1997, XP002098935 * abstract * -----	7-9	TECHNICAL FIELDS SEARCHED (Int.Cl.6)

EPO FORM 1503 03.82 (P04C10)